In the Claims

Please amend and add the following claims according to the following listing of claims under 37 CFR 1.121. Please amend allowed claim 3. Please reinstate canceled previously canceled claim 97 as claim 102. Please add new claims 103 to 159.

Listing of Claims under 37 CFR 1.121 (revised):

1-2 (CANCELED)

3. (CURRENTLY AMENDED): A process for identifying one or more bi-allelic markers linked to a bi-allelic ~~genetic characteristic gene~~ trait-causing polymorphism in a species of creatures, comprising the acts of:

a) choosing two or more bi-allelic covering markers so that a CL-F region is systematically covered by the two or more covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency;

b) choosing a statistical linkage test based on allelic association for each covering marker;

c) choosing a sample of individuals for each covering marker ;

d) obtaining genotype data/sample allele frequency data for each covering marker and the sample chosen for each covering marker, and obtaining phenotype status data for the ~~genetic characteristic~~ trait for each individual in the sample chosen for each covering marker;

e) calculating evidence for linkage between each covering marker and the gene using the statistical linkage test based on allelic association chosen for each covering marker and the genotype data/sample allele frequency data for each covering marker and using the phenotype status data for the ~~genetic characteristic~~ trait for each individual in the sample chosen for each covering marker obtained in d); and

f) identifying those covering markers as linked to the ~~genetic characteristic gene~~ trait-causing polymorphism which show evidence for linkage based on the calculations of e).

4. (ORIGINAL): A process as in claim 3, wherein the CL-F region is N covered to within a CL-F distance δ by the two or more bi-allelic covering markers, so that each point in the region is within the CL-F distance δ of N or more of the covering markers, wherein δ is equal to about [δ_{CL}, 0.25] or the

equivalent thereof, δ_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

5. (ORIGINAL): A process as in claim 4, wherein the CL-F region includes 81 percent or more of the centerpoints of the matrix centerpoint lattice of a CL-F matrix, the number of cells in the matrix being greater than or equal to three, wherein the matrix has R rows and C columns, each cell of the matrix being of length L_{MC} and width W_{MC}, and L_{MC} being less than or equal to about $2\delta_{CL}$, and W_{MC} being less than or equal to 0.5, δ_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, there being N or more covering markers in each cell of 81 percent or more of the cells of the matrix, N is an integer greater than or equal to 1; the covering markers being distributed over a chromosomal region of interest, the region of interest being approximately the smallest chromosome interval that contains all of the covering markers, and the covering markers comprising essentially less than all of the polymorphisms in the region of interest.

6-7 (CANCELED)

8. (ORIGINAL): A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

9-19 (CANCELED)

20. (PREVIOUSLY AMENDED): A process as in claim 3, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

21. (PREVIOUSLY AMENDED): A process as in claim 20, wherein the process comprises the use of a computer program.

22-32 (CANCELED)

33. (ORIGINAL): A process for obtaining genotype data/sample allele frequency data for each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, each individual in the sample being a member of the same species,

comprising:

a)determining information on the presence or absence of each allele of each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, a CL-F region being systematically covered by the two or more bi-allelic covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency; and

b) transforming the information of step a) into genotype data/sample allele frequency data for each marker of the group.

34. (ORIGINAL): A process for obtaining genotype data/sample allele frequency data as in claim 33, wherein the CL-F region is N covered to within a CL-F distance δ by the two or more bi-allelic covering markers, so that each point in the region is within the CL-F distance δ of N or more of the covering markers, wherein δ is equal to about [δ_{CL}, 0.25] or the equivalent thereof, δ_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

35. (ORIGINAL): A process for obtaining genotype data/sample allele frequency data as in claim 34, wherein the CL-F region includes 81 percent or more of the centerpoints of the matrix centerpoint lattice of a CL-F matrix, the number of cells in the matrix being greater than or equal to three, wherein the matrix has R rows and C columns, each cell of the matrix being of length L_{MC} and width W_{MC}, and L_{MC} being less than or equal to about $2\delta_{CL}$, and W_{MC} being less than or equal to 0.5, δ_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, there being N or more covering markers in each cell of 81 percent or more of the cells of the matrix, N is an integer greater than or equal to 1; the covering markers being distributed over a chromosomal region of interest, the region of interest being approximately the smallest chromosome interval that contains all of the covering markers, and the covering markers comprising essentially less than all of the polymorphisms in the region of interest.

36-37 (CANCELLED)

38. (ORIGINAL): A process for obtaining genotype data/sample allele frequency data as in claim 35, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein there is a subgroup of one or more of the covering markers, and

each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

39-49 (CANCELLED)

50. (PREVIOUSLY AMENDED): A process for obtaining genotype data/sample allele frequency data as in claim 33, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

51. (PREVIOUSLY AMENDED): A process for obtaining genotype data/sample allele frequency data as in claim 50, wherein the process comprises the use of a computer program.

52-77 (CANCELLED)

78. (ORIGINAL): One or more copies of a set of oligonucleotides, the set of oligonucleotides being substantially complementary to a group of two or more bi-allelic covering markers of the same species, wherein the group of covering markers systematically cover a CL-F region, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency.

79. (ORIGINAL): One or more copies of a set of oligonucleotides as in claim 78, wherein the CL-F region is N covered to within a CL-F distance δ by the two or more bi-allelic covering markers, so that each point in the region is within the CL-F distance δ of N or more of the covering markers, wherein δ is equal to about [δ_{CL}, 0.25] or the equivalent thereof, δ_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

80. (ORIGINAL): One or more copies of a set of oligonucleotides as in claim 78, wherein the CL-F region includes 81 percent or more of the centerpoints of the matrix centerpoint lattice of a CL-F matrix, the number of cells in the matrix being greater than or equal to three, wherein the matrix has R rows and C columns, each cell of the matrix being of length L_{MC} and width W_{MC}, and L_{MC} being less than or equal to about $2\delta_{CL}$, and W_{MC} being less than or equal to 0.5, δ_{CL} is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, there being N or more covering markers in each cell of 81 percent or more of the cells of the matrix, N is an integer greater than or equal to 1; the covering markers being distributed over a chromosomal region of interest, the region of interest being approximately the smallest chromosome interval that contains all of the covering markers, and

the covering markers comprising essentially less than all of the polymorphisms in the region of interest.

81-82 (CANCELED)

83. (ORIGINAL): One or more copies of a set of oligonucleotides as in claim 80, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

84-94 (CANCELED)

95. (PREVIOUSLY AMENDED): One or more copies of a set of oligonucleotides as in claim 78, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

99. (PREVIOUSLY ADDED): A process as in claim 4, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

100. (PREVIOUSLY ADDED): A process for obtaining genotype data/sample allele frequency data as in claim 34, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

101. (PREVIOUSLY ADDED): One or more copies of a set of oligonucleotides as in claim 79, wherein there is a subgroup of the covering markers, and the markers in the subgroup are a majority of the covering markers, and each marker in the subgroup is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

102. (REINSTATED—PREVIOUSLY CLAIM 97): An apparatus for obtaining genotype data/sample allele frequency data for each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, each individual in the sample being a member of the same species, comprising:

a) means for determining information on the presence or absence of each allele of each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more

individuals of a sample, a CL-F region being systematically covered by the two or more bi-allelic covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency; and

b) means for transforming the information of means a) into genotype data/sample allele frequency data for each marker of the group.

103. (NEW): A process as in claim 3, wherein the CL-F region is for a species and a population and the population is a group of individuals as in the field of population genetics, wherein the covering markers are chosen with attention to marker allele frequency and the choice of covering markers uses marker allele frequency to increase the power of an association based linkage test to detect evidence for linkage, wherein the choice of covering markers is not based on the assumption that a covering marker is the trait-causing polymorphism.

104. (NEW): A process as in claim 103, wherein the CL-F region is N-covered to within [x,y], wherein x is any one of i) through iv) inclusive: i) less than or equal to about the greatest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, ii) about 10 to 12 cM or an equivalent thereof , iii) less than or equal to about 1 million bp or an equivalent thereof, iv) less than or equal to about 250,000 bp or an equivalent thereof and y is about 0.2 and $N \geq 1$.

105. (NEW): A process as in claim 104, wherein the chromosomal distance x is short enough that polymorphisms within x of each other are likely to be in linkage disequilibrium with each other.

106. (NEW): A process as in claim 104, wherein the chromosomal location coordinates of the CL-F region range over a chromosome or a subregion of interest and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located on the chromosome or in the subregion of interest and within the subrange or range is in the CL-F region, wherein the chromosome or the subregion of interest is completely covered by chromosomal segments, wherein the segments may or may not overlap, wherein the segments are short enough that polymorphisms within each segment are likely to be in linkage disequilibrium with each other, wherein the length of each segment is less than or equal to 7 to 10 cM, or wherein the length of each segment is less than 1 cM, wherein x is less than or equal to the length of each segment.

107. (NEW): A process as in claim 104, wherein the least common allele frequency coordinates of the CL-F region range over the subrange 0 to 0.2, and the CL-F region is N covered to within [x, y] and y is 0.15 so that each covering marker is within the subrange 0 to 0.35, wherein a conventional marker map to achieve high heterozygosity of the markers in the map (so that the least common allele frequencies of the markers in the map are preferentially near 0.5) is not chosen.

108. (NEW): A process as in claim 104, wherein the CL-F region is N covered to within [x,y], wherein x is less than or equal to about 250,000 bp or an equivalent thereof and y is less than or equal to about 0.2.

109. (NEW): A process as in claim 107, wherein the species is human being, wherein the chromosomal distance x is short enough that polymorphisms within x of each other are likely to be in linkage disequilibrium with each other.

110. (NEW): A process as in claim 104, wherein the chromosomal location coordinates of the CL-F region range over an entire gene structure and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located in the entire gene structure and within the subrange or range is in the CL-F region.

111. (NEW): A process as in claim 104, wherein the chromosomal location coordinates of the CL-F region range over a gene region, and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located in the gene region and within the subrange or range is in the CL-F region, wherein the term "gene region" is used in the sense the term "gene region" is used in the term "insulin gene region" and wherein the term "gene" in the term "gene region" does not mean a trait-causing polymorphism.
112. (NEW): A process as in claim 106, wherein the subregion of interest is a gene region, wherein the term "gene region" is used in the sense the term "gene region" is used in the term "insulin gene region" and wherein the term "gene" in the term "gene region" does not mean a trait-causing polymorphism.

113. (NEW): A process as in claim 105, wherein the species is human being, wherein the CL-F region is N covered to within [x,y], wherein y is 0.2.

114. (NEW): A process as in claim 109, wherein $N \geq 2$, and the number of covering markers is 12 or more.

115. (NEW): A process as in claim 112, wherein $N \geq 2$, wherein the species is human being, wherein the CL-F region is a segment-subrange, wherein the segment of the segment-subrange is the region of interest, wherein the region of interest is a gene region, wherein the subregion of interest is completely covered by chromosomal segments, wherein the segments may or may not overlap, wherein the segments are short enough that polymorphisms within each segment are likely to be in linkage disequilibrium with each other, wherein the length of each segment is less than 1 cM, wherein each covering marker belongs to a subset of covering markers, wherein there is more than one marker in each subset, wherein the markers in each subset have approximately the same allele frequencies, wherein the markers in each subset are located within one segment and within each segment there are one or more subsets of covering markers, wherein the subrange of the segment-subrange is the subrange 0 to 0.1 so that each covering marker is within the subrange 0 to about 0.3, wherein the least common allele frequency of one or more covering markers is less than 0.2, wherein the number of covering markers is 12 or more, wherein a conventional marker map to achieve high heterozygosity of the markers in the map (so that the least common allele frequencies of the markers in the map are preferentially near 0.5) is not chosen.

116. (NEW): A process as in claim 115, wherein no two covering markers in the same subset provide nearly identical information with respect to their linkage and association with a third polymorphism.

117. (NEW): A process as in claim 116, wherein each covering marker is an SNP.

118. (NEW): A process as in claim 114, wherein each covering marker is an SNP.

119. (NEW): A process as in claim 108, wherein the CL-F region is a segment-subrange, wherein the subrange of the segment-subrange is the subrange 0 to 0.1 so that each covering marker is within the subrange 0 to about 0.3, wherein a conventional marker map to achieve high heterozygosity of the markers in the map (so that the least common allele frequencies of the markers in the map are preferentially near 0.5) is not chosen.

120. (NEW): A process as in claim 108, wherein the chromosomal location coordinates of the CL-F region range over an entire gene structure and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located in the entire gene structure and within the subrange or range is in the CL-F region.

121. (NEW): A process as in claim 119, wherein the species is human being.

122. (NEW): A process as in claim 119, wherein the segment of the segment-subrange includes an entire gene structure, wherein the CL-F region is N-covered to within [x,y] and y =0.1.

123. (NEW): A process as in claim 119, wherein the segment of the segment-subrange is a gene

region, wherein the term "gene region" is used in the sense the term "gene region" is used in the term "insulin gene region" and wherein the term "gene" in the term "gene region" does not mean a trait-causing polymorphism.

124. (NEW): A process as in claim 119, wherein $N \geq 2$ and the number of covering markers is 12 or more.

125. (NEW): A process as in claim 119, wherein the least common allele frequency of one or more covering markers is less than 0.2.

126. (NEW): A process as in claim 119, wherein the chromosomal distance x is short enough that polymorphisms within x of each other are likely to be in linkage disequilibrium with each other.

127. (NEW): A process as in claim 103, wherein the CL-F region is N-covered to within [x,y], wherein x is any one of i) through iv) inclusive: i) less than or equal to about the greatest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, ii) about 10 to 12 cM or an equivalent thereof , iii) less than or equal to about 1 million bp or an equivalent thereof, iv) less than or equal to about 250,000 bp or an equivalent thereof and y is 0.2 and $N \geq 1$.

128. (NEW): A process as in claim 127, wherein the number of covering markers is 8 or more.

129. (NEW): A process as in claim 127, wherein the chromosomal location coordinates of the CL-F region range over an entire chromosome and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located on the chromosome and within the subrange or range is in the CL-F region or wherein the CL-F region is a segment-subrange.

130. (NEW): A process as in claim 127, wherein the chromosomal distance x is short enough that polymorphisms within x of each other are likely to be in linkage disequilibrium with each other.

131. (NEW): A process as in claim 127, wherein the species is human being.

132. (NEW): A process as in claim 127, wherein the chromosomal location coordinates of the CL-F region range over an entire gene structure and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located in the entire gene structure and within the subrange or range is in the CL-F region.

133. (NEW): A process as in claim 127, wherein the chromosomal location coordinates of the CL-F region are in one or more genes, wherein the term "gene" is used in the term's usual sense, wherein the term "gene" does not mean a trait-causing polymorphism.

134. (NEW): A process as in claim 3, wherein the CL-F region is N-covered to within [x,y], wherein x is any one of i) through iv) inclusive: i) less than or equal to about the greatest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, ii) about 10 to 12 cM or an equivalent thereof , iii) less than or equal to about 1 million bp or an equivalent thereof, iv) less than or equal to about 250,000 bp or an equivalent thereof and y is 0.25 and $N \geq 1$; further comprising the act of:

f)localizing the trait-causing polymorphism to the chromosomal location-least common allele frequency (CL-F) location of one or more markers that show evidence for linkage based on the calculations of act e), wherein the localizing uses a technique or techniques that detects gradients, wherein the detection technique or techniques uses a gradient along the allele frequency dimension.

135. (NEW): A process as in claim 134, wherein the detection technique or techniques uses a computer.

136. (NEW): A process as in claim 134, wherein the chromosomal location coordinates of the CL-F

region ranges over an entire chromosome or over all the chromosomes of the species and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located on the chromosome or a chromosome and within the subrange or range is in the CL-F region.

137. (NEW): A process as in claim 135, wherein the chromosomal location coordinates of the CL-F region ranges over an entire chromosome or over all the chromosomes of the species and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located on the chromosome or within a chromosome and within the subrange or range is in the CL-F region.

138. (NEW): A process as in claim 104, wherein the CL-F region is a collection of one or more CL-F points, wherein each point in the CL-F region is the location of a known polymorphism that is a possible trait-causing polymorphism, wherein each possible trait-causing polymorphism has the characteristic described in (1): (1) any one possible trait causing polymorphism in the CL-F region is in linkage disequilibrium with a covering marker that is within [x,y] of the one trait-causing polymorphism.

139. (NEW): A process as in claim 138, wherein each possible trait-causing polymorphism has the characteristic described in (1): (1) any one possible trait causing polymorphism in the CL-F region is in positive linkage disequilibrium with a covering marker that is within [x,y] of the one trait-causing polymorphism.

140. (NEW): A process as in claim 139, wherein the positive linkage disequilibrium is greater than or equal to 1/2 δ_{max}.

141. (NEW): A process as in claim 104, wherein the CL-F region is a collection of one or more CL-F points, wherein each point in the CL-F region is the location of a known polymorphism that is a possible trait-causing polymorphism, wherein there is increased power of an association-based linkage test to detect evidence for linkage between each of one or more of the covering markers and the trait when the trait-causing polymorphism is located at a point in the CL-F region, wherein each possible trait-causing polymorphism has the characteristic described in (1):

(1) for any one possible trait-causing polymorphism the increased power to detect evidence for linkage of a covering marker and the trait is increased compared to the power to detect evidence for linkage of an other marker and the trait, wherein the increased power is quantified by a difference between a mean χ^2_{tdt} calculation for the covering marker and a mean χ^2_{tdt} calculation for the other marker, wherein each of the two mean χ^2_{tdt} calculations uses r = 5, additive mode of inheritance and sample size of 200 hundred families with 2 affected sibs; wherein each of the two mean χ^2_{tdt} calculations equals $800(H/F)\ (2\ P_t - 1)^2$; wherein the values of (H/F) and P_t used in each mean χ^2_{tdt} calculation are for an allele of the covering marker and an allele of the possible trait-causing polymorphism or are for an allele of the other marker and the allele of the possible trait-causing polymorphism respectively; wherein the disequilibrium between the covering marker and the possible trait-causing polymorphism is not greater than the disequilibrium between the other marker and the possible trait-causing ploymorphism when each of the two disequilibria is computed respectively as δ/δ_{max} for $\delta \geq 0$ or δ/δ_{min} for $\delta < 0$, wherein each of the δ values is a coefficient of disequilibrium.

142. (NEW): A process as in claim 103, wherein the CL-F region is a collection of one or more CL-F points, wherein there is increased power of an association-based linkage test to detect evidence for linkage between each of one or more of the covering markers and the trait when the trait-causing polymorphism is located at a point in the CL-F region, wherein each possible trait-causing polymorphism has the characteristic described in (1):

(1) for any one possible trait-causing polymorphism the increased power to detect evidence for linkage of a covering marker and the trait is increased compared to the power to detect evidence for linkage of an other marker and the trait, wherein the increased power is quantified by a difference between a

mean χ^2_{tdt} calculation for the covering marker and a mean χ^2_{tdt} calculation for the other marker, wherein each of the two mean χ^2_{tdt} calculations uses r = 5, additive mode of inheritance and sample size of 200 hundred families with 2 affected sibs; wherein each of the two mean χ^2_{tdt} calculations equals $800(H/F)\ (2\ P_t - 1)^2$; wherein the values of (H/F) and P_t used in each mean χ^2_{tdt} calculation are for an allele of the covering marker and an allele of the possible trait-causing polymorphism or are for an allele of the other marker and the allele of the possible trait-causing polymorphism respectively; wherein the disequilibrium between the covering marker and the possible trait-causing polymorphism is not greater than the disequilibrium between the other marker and the possible trait-causing ploymorphism when each of the two disequilibria is computed respectively as δ/δ_{max} for $\delta \geq 0$ or δ/δ_{min} for $\delta < 0$, wherein each of the δ values is a coefficient of disequilibrium, wherein m is the allele frequency of the allele of the covering marker, wherein p is the allele frequency of the allele of the possible trait-causing polymorphism, and wherein the m/p ratio departs from unity or δ is not close to δ_{max}.

143. (NEW): An apparatus as in claim 142, wherein the m/p ratio departs from unity or δ is not close to δ_{max}, and wherein the difference between the allele frequencies m and p is greater than or equal to 0.1.

144. (NEW): An apparatus as in claim 142, wherein the difference between the allele frequencies m and p is greater than or equal to 0.05 or δ is not close to δ_{max}.

145. (NEW): A process for obtaining genotype/sample allele frequency data as in claim 33, wherein the CL-F region is for a species and a population and the population is a group of individuals as in the field of population genetics, wherein the covering markers are chosen with attention to marker allele frequency and the choice of covering markers uses marker allele frequency to increase the power of an association based linkage test to detect evidence for linkage, wherein a conventional marker map to achieve high heterozygosity of the markers in the map (so that the least common allele frequencies of the markers in the map are preferentially near 0.5) is not chosen, wherein the choice of covering markers is not based on the assumption that a covering marker is the trait-causing polymorphism.

146. (NEW): A process as in claim 145, wherein the CL-F region is N-covered to within [x,y], wherein x is any one of i) through iv) inclusive: i) less than or equal to about the greatest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, ii) about 10 to 12 cM or an equivalent thereof , iii) less than or equal to about 1 million bp or an equivalent thereof, iv) less than or equal to about 250,000 bp or an equivalent thereof and y is about 0.2 and $N \geq 1$.

147. (NEW): A process as in claim 146, wherein the chromosomal distance x is short enough that polymorphisms within x of each other are likely to be in linkage disequilibrium with each other.

148. (NEW): A process as in claim 146, wherein the chromosomal location coordinates of the CL-F region range over a chromosome or a subregion of interest and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located on the chromosome or in the subregion of interest and within the subrange or range is in the CL-F region, wherein the chromosome or the subregion of interest is completely covered by chromosomal segments, wherein the segments may or may not overlap, wherein the segments are short enough that polymorphisms within each segment are likely to be in linkage disequilibrium with each other, wherein the length of each segment is less than or equal to 7 to 10 cM, or wherein the length of each segment is less than 1 cM, wherein x is less than or equal to the length of each segment.

149. (NEW): A process as in claim 146, wherein the least common allele frequency coordinates of the CL-F region range over the subrange 0 to 0.2, and the CL-F region is N covered to within [x, y] and y is 0.15 so that each covering marker is within the subrange 0 to 0.35.

150. (NEW): A process as in claim 146, wherein the CL-F region is N covered to within [x,y], wherein x is less than or equal to about 250,000 bp or an equivalent thereof and y is less than or equal to about 0.2.

151. (NEW): A process as in claim 149, wherein the species is human being, wherein the chromosomal distance x is short enough that polymorphisms within x of each other are likely to be in linkage disequilibrium with each other.

152. (NEW): A process as in claim 146, wherein the chromosomal location coordinates of the CL-F region range over an entire gene structure and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located in the entire gene structure and within the subrange or range is in the CL-F region.

153. (NEW): A process as in claim 146, wherein the chromosomal location coordinates of the CL-F region range over a gene region, and the least common allele frequency coordinates range over a subrange or the range 0 to 0.5 so that each CL-F point located in the gene region and within the subrange or range is in the CL-F region, wherein the term "gene region" is used in the sense the term "gene region" is used in the term "insulin gene region" and wherein the term "gene" in the term "gene region" does not mean a trait-causing polymorphism.

154. (NEW): A process as in claim 148, wherein the subregion of interest is a gene region, wherein the term "gene region" is used in the sense the term "gene region" is used in the term "insulin gene region" and wherein the term "gene" in the term "gene region" does not mean a trait-causing polymorphism.

155. (NEW): A process as in claim 147, wherein the species is human being, wherein the CL-F region is N covered to within [x,y], wherein y is 0.2.

156. (NEW): A process as in claim 151, wherein $N \geq 2$, and the number of covering markers is 12 or more.

157. (NEW): A process as in claim 154, wherein $N \geq 2$, wherein the species is human being, wherein the CL-F region is a segment-subrange, wherein the segment of the segment-subrange is the region of interest, wherein the region of interest is a gene region, wherein the subregion of interest is completely covered by chromosomal segments, wherein the segments may or may not overlap, wherein the segments are short enough that polymorphisms within each segment are likely to be in linkage disequilibrium with each other, wherein the length of each segment is less than 1 cM, wherein each covering marker belongs to a subset of covering markers, wherein there is more than one marker in each subset, wherein the markers in each subset have approximately the same allele frequencies, wherein the markers in each subset are located within one segment and within each segment there are one or more subsets of covering markers, wherein the subrange of the segment-subrange is the subrange 0 to 0.1 so that each covering marker is within the subrange 0 to about 0.3, wherein the least common allele frequency of one or more covering markers is less than 0.2, wherein the number of covering markers is 12 or more.

158. (NEW): A process as in claim 157, wherein no two covering markers in the same subset provide nearly identical information with respect to their linkage and association with a third polymorphism.

159. (NEW): A process as in claim 158, wherein each covering marker is an SNP.